

SEQUENCE LISTING

<110> Armstrong, Katherine
 Hey, Timothy D
 Folkerts, Otto
 Smith, Kelley A
 Hopkins, Nicole L

<120> MAIZE MIP SYNTHASE PROMOTER

<130> 50597

<140>

<141>

<150> US 60/168,612

<151> 1999-12-02

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 1959

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (137)..(1699)

<400> 1

```

gaattcggca caagcaaagg agcgcgggcgg cccctccttc cttcctccca cttctctcgc 60
gcggcgcctcg cttacctcgc ctgcattcc gttcgagcag gggagcggca gtgagaaggg 120
aggggaattaa ggcaag atg ttc atc gag agc ttc cgc gtc gag agc ccc cac 172
      Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His
        1             5             10

gtg cgg tac ggc ccg acg gag atc gag tcg gag tac cgg tac gac acg 220
Val Arg Tyr Gly Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr
      15             20             25

acg gag ctg gtg cac gag gcc aag gac ggc gcc tcc cgc tgg gtc gtc 268
Thr Glu Leu Val His Glu Ala Lys Asp Gly Ala Ser Arg Trp Val Val
      30             35             40

cgc ccc aag tcc gtc aag tac aac ttc cgg acc agc acc gcg gtc ccc 316
Arg Pro Lys Ser Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro
      45             50             55             60

aag ctc ggg gtc atg ctt gtg ggg tgg gga ggc aac aac ggg tcc acg 364
Lys Leu Gly Val Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr
      65             70             75

ctg acg gct ggg gtc att gcc aac agg gag ggg atc tca tgg gcg acc 412

```

Leu Thr Ala Gly Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr
 80 85 90
 aag gac aag gtg cag caa gcc aac tac tac ggc tcc ctc acc cag gct 460
 Lys Asp Lys Val Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala
 95 100 105
 tcc acc atc aga gta ggc agc tac aac ggg gag gag ata tat gcg ccg 508
 Ser Thr Ile Arg Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro
 110 115 120
 ttc aag agc ctc cta ccc atg gtg aac cca gac gac ctt gtg ttt gga 556
 Phe Lys Ser Leu Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly
 125 130 135 140
 ggc tgg gac atc agc agc atg aac ctg gca gat gcc atg acc agg gcc 604
 Gly Trp Asp Ile Ser Ser Met Asn Leu Ala Asp Ala Met Thr Arg Ala
 145 150 155
 aag gtg ctg gac att gac ctg cag aag cag ctc agg ccc tac atg gag 652
 Lys Val Leu Asp Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu
 160 165 170
 tcc atg gtg cca ctt ccc ggt gtc tat gat ccg gac ttc atc gcc gct 700
 Ser Met Val Pro Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala
 175 180 185
 aac cag ggc tct cgt gcc aac aat gtc atc aag ggc acc aag aaa gaa 748
 Asn Gln Gly Ser Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu
 190 195 200
 cag gtg gag cag atc atc aaa gat atc agg gag ttt aag gag aag aac 796
 Gln Val Glu Gln Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn
 205 210 215 220
 aaa gtg gac aag gta gtt gtg ctg tgg act gca aac act gaa agg tac 844
 Lys Val Asp Lys Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr
 225 230 235
 agc aat gta tgt gct ggt ctc aac gac aca atg gag aat ctg ctg gca 892
 Ser Asn Val Cys Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala
 240 245 250
 tct gtg gac aag aac gag gcg gag atc tcg cca tca aca cta tat gcc 940
 Ser Val Asp Lys Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala
 255 260 265
 att gcc tgt gtc acg gag ggg gtg ccg ttc atc aat ggg agc ccc cag 988
 Ile Ala Cys Val Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln
 270 275 280
 aac act ttt gtg cct ggg ctg att gat ctt gct atc aag aac aac tgc 1036
 Asn Thr Phe Val Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys
 285 290 295 300
 ctg atc ggt ggt gac gac ttc aag agt ggg cag acc aag atg aaa tcg 1084
 Leu Ile Gly Gly Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser
 305 310 315
 gtc ctg gtt gat ttt ctt gtt ggt gct gga ata aag ccc acc tcg att 1132
 Val Leu Val Asp Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile

320 325 330
 gtg agc tac aac cac ttg gga aac aac gac ggc atg aac ctg tct gcc 1180
 Val Ser Tyr Asn His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala
 335 340 345
 cct caa aca ttc agg tcc aag gag atc tcc aag agc aac gtg gtg gat 1228
 Pro Gln Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp
 350 355 360
 gac atg gtc tca agc aat gcc att ctc tat ggg ccc ggc gag cat ccc 1276
 Asp Met Val Ser Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro
 365 370 375 380
 gat cat gtt gtt gtc atc aag tat gtg ccg tat gtg gga gac agt aag 1324
 Asp His Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys
 385 390 395
 agg gct atg gac gag tac aca tca gag atc ttc atg ggc ggc aag agc 1372
 Arg Ala Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser
 400 405 410
 acc atc gtg ctg cac aac acc tgc gag gac tcg ctc ctc gcc gca ccg 1420
 Thr Ile Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro
 415 420 425
 atc atc ctc gat ctg gtg ctc ctg gct gag ctc agc acc agg atc cag 1468
 Ile Ile Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln
 430 435 440
 tta aaa cct gag gga acg gac aag ttc cac tcc ttc cac ccg gtg gcc 1516
 Leu Lys Pro Glu Gly Thr Asp Lys Phe His Ser Phe His Pro Val Ala
 445 450 455 460
 acc atc ctt agc tac ctc acc aag gca cca ctg gtt cca ccc ggc aca 1564
 Thr Ile Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr
 465 470 475
 ccg gtg gtg aac gct ctt gca aag cag agg gcg atg ctg gag aac atc 1612
 Pro Val Val Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile
 480 485 490
 atg agg gct tgc gtt ggc ctg gcc cca gag aac aac atg atc ctg gag 1660
 Met Arg Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu
 495 500 505
 tac aag tga gcg aag tgg cgt ggc ctg cag cta gat atg gaggaggctg 1709
 Tyr Lys
 510
 cacgaagggg actagagagg cgagattagc tgtggaattg tgttggttc tcgtgttttc 1769
 ttttgcgttc ttttcctggt catcgctgtg gcgcttttgt attttatttg ttggaccogt 1829
 aacactatca gggctctgct attagcgctt gaagcctgta atggcattgg catcgatatga 1889
 taatgtgata gaggggtgcta gttcccctaa aaaaaaaaaa aaaaaaaac tcgagggggg 1949
 gcccggtacc 1959

<210> 2
 <211> 510
 <212> PRT
 <213> Zea mays

<400> 2

```

Met Phe Ile Glu Ser Phe Arg Val Glu Ser Pro His Val Arg Tyr Gly
  1           5           10           15

Pro Thr Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu Val
          20           25           30

His Glu Ala Lys Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys Ser
      35           40           45

Val Lys Tyr Asn Phe Arg Thr Ser Thr Ala Val Pro Lys Leu Gly Val
      50           55           60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
      65           70           75           80

Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
          85           90           95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
          100          105          110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
      115          120          125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
      130          135          140

Ser Ser Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp
      145          150          155          160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val Pro
          165          170          175

Leu Pro Gly Val Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Gly Ser
          180          185          190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Val Glu Gln
          195          200          205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Asn Lys Val Asp Lys
      210          215          220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val Cys
      225          230          235          240

Ala Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp Lys
          245          250          255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
          260          265          270

Thr Glu Gly Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
          275          280          285

Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly Gly

```

290 295 300
 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
 305 310 315 320
 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
 325 330 335
 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
 340 345 350
 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Ser
 355 360 365
 Ser Asn Ala Ile Leu Tyr Gly Pro Gly Glu His Pro Asp His Val Val
 370 375 380
 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
 385 390 395 400
 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
 405 410 415
 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
 420 425 430
 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Pro Glu
 435 440 445
 Gly Thr Asp Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460
 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480
 Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495
 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
 500 505 510

<210> 3
 <211> 2069
 <212> DNA
 <213> Zea mays

<400> 3
 tctagatttt ttttcaattc accccgagta aatatccaat cacaatctaa aaatcaggag 60
 aaattatatg gccatattat agaagcaact aaataaaatg tgcgttgat tgaaaaaaa 120
 acctatttat aacaaacatc tgccaagaat acaattcttt tatacacaac ttatatgtga 180
 gttctttttt tcttgtaact cttattaata aaacattttt ggctattaaa taatggcaac 240
 taagtttagc ccaactgtaat tagattttgt ctggaacaat ttctctgact aagaagctat 300
 ttggactgtc cttttgcaa acaagtagaa aatggaaccg ctccttaaaa aaccattctc 360

acatcgctgg gtgctgaata aaactgaaaa cattagcttt ttatagctct cgctctctgc 420
 tagtatgtgt tataaaatca ttttaccat taccttttta aataactgta cgtagtttca 480
 tcagtagaac tactcacgga gctaaaacaa aaaaagttgt tctactgata aaagcagaga 540
 tgatgtatga ccgtgaccgt gagctaaagt ccaaaaaaaaa aaactgctcc acaataacga 600
 caaaacaaag ttgtattgta tggcctaaat tacagcacac tgacaccaca cgtatattat 660
 tctctctcca ttatcacagg atgtaactgt aaaaattttg tatgttaaac attttagta 720
 aatattgcta gcatttacgt ctacggaatt tattgaaaaa atgtagtatt gttttatata 780
 attttaataa aactgtaaat cgtctggctt cgtttctgga tggaggataa atagtgaata 840
 cgaatgggaa acaccacaac aaccacgccg ctgcgttctg cgaatcacat gagcgatcag 900
 tgccttgctg ttccgtgaac ttgcacgcaa ggacgagagc ctttctgcct ttgcatgcaa 960
 ggacaagagt ctttacatgc aaggacaaat aactcccacg cgccccaccg tgctttggca 1020
 agccacatgg caccctgccg atcacaattc acaggcccag gcttccggtg gtcgctgccc 1080
 gtgagtctga caccgcacca catggccgcc gtaggcgctg cctacgcacc aaggcgactc 1140
 gtggtgccag gctctcggcg gctttggagt cggtgccatg ccgcggggtc cgtggaccgc 1200
 tcctaggggc caggacgaag ctgcaccgca caagcggggc gcgctgact ccgtgaccgt 1260
 gaggcgggag taaccaggag ctcccgccac gcttgagacc acgtgacggc gcagaggagc 1320
 tccacgcgat caaaagcgcc cgccacttct aaaggtcagg ggtcttgct tctgcccctc 1380
 gtgcttccct caaattctgg acctagtggg tcaatttacg tacacctcag caaccgatgc 1440
 agccagtatg atgagcacga ttgtgacgtg ttgggggtca tggcfaatgg caaccgagca 1500
 cgaattggta gtgtctgctt tttgtacacg tgatagcatt tgattcgttc attcaatttg 1560
 aactgtttaa acttatatat gtagagaaat tagtccaact catgcttaat aaaaagtata 1620
 aaaccatcg aatttatgaa ttatgatagc aggtatccta tccattgtca tcgctcacag 1680
 tcacagaggt agccactgcc gacggccgac ggcctcccat ttcgctccc tctactcct 1740
 atgctgcggt ccagcaaaaag ttccgggcctt ccggcaatcc gccggcgccc gtcggctcaa 1800
 atcgcatcta ccgcggctag aagctctctc ttctccctc cgatccggtg gggctccattt 1860
 ccttcaattg tggcagtggc cgtctcgaac cctctataaa tccccacccc cggacaccc 1920
 tccccacca cacagcccaa caacaaggag ccggcgggcc cctccttct tctccact 1980
 tctctcgcgc ggcgctcgt tacctcgctt cgcattcgt tcgagcaggg gagcggcagt 2040
 gagaagggag ggaattaagg caaccatgg 2069